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Article

Novel common genetic susceptibility loci for colorectal cancer

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Abbreviations

1KGP	1000 Genomes Project
ACCC	Asia Colorectal Cancer Consortium
ChIP-Seq	Chromatin immunoprecipitation and sequencing
CORECT	Colorectal Transdisciplinary Study
CRC	Colorectal cancer
ENCODE	ENCyclopedia Of DNA Elements
eQTL	Expression quantitative trait locus
GECCO	Genetics and Epidemiology of Colorectal Cancer Consortium
GTEx	Genotype-tissue expression
GWAS	Genome-wide association study
LD	Linkage disequilibrium
MAF	Minor allele frequency
MEC	Multiethnic cohort
OR	Odds ratio
PC	Principal component
PCA	Principal components analysis
QC	Quality control
SIGMA	Slim Initiative in Genomic Medicine for the Americas

Keywords

Colorectal cancer; colon cancer; rectal cancer; epidemiology; GWAS; genetics; genome-wide association study; risk factor; genetic epidemiology; variant; susceptibility

Abstract

Background: Previous genome-wide association studies (GWAS) have identified 42 loci ($P<5x10^{-8}$) associated with the risk of colorectal cancer (CRC). Expanded consortium efforts facilitating the discovery of additional susceptibility loci may capture unexplained familial risk.

Methods: We conducted a GWAS in European-descent CRC cases and controls using a discovery-replication design, followed by examination of novel findings in a multiethnic sample (cumulative N=163,315). In the discovery stage (36,948 cases/30,864 controls), we identified genetic variants with minor allele frequency ≥1% associated with risk of CRC using logistic regression followed by a fixed effects inverse variance weighted meta-analysis. All novel independent variants reaching genome-wide statistical significance (two-sided $P<5x10^{-8}$) were tested for replication in separate European-ancestry samples (12,952 cases/48,383 controls). Next, we examined the generalizability of discovered variants in East Asians, African-Americans, and Hispanics (12,085 cases/22,083 controls). Finally, we examined the contributions of novel risk variants to familial relative risk and examined the prediction capabilities of a polygenic risk score. All statistical tests were two-sided.

Results: The discovery GWAS identified eleven variants associated with CRC at $P<5x10^{-8}$, of which nine (at 4q22.2/5p15.33/5p13.1/ 6p21.31/6p12.1/10q11.23/12q24.21/16q24.1/ 20q13.13) independently replicated at $P<0.05$. Multiethnic follow-up supported the generalizability of discovery findings. These results provide a 14.7% increase in familial relative risk explained by common risk alleles from 10.3% (95% CI 7.9 – 13.7%; known variants) to 11.85% (95% CI 9.2 – 15.5%; known and novel variants)**.** A polygenic risk score identifies 4.3% of the population at an odds ratio of at least 2.0.

Conclusions: This study provides insight into the architecture of common genetic variation

contributing to CRC etiology and improves risk prediction for individualized screening.

Background

Colorectal cancer (CRC) is a complex polygenetic disease, and heritability accounts for up to 35% of the variation in risk of developing CRC [1, 2]. Some of this heritability is attributable to rare high-penetrance alleles associated with cancer syndromes, now routinely incorporated into clinical care. In addition, genome-wide association studies (GWAS) have identified variation in numerous regulatory regions and other genomic loci that contribute quantifiable risks for CRC development. Specifically, GWAS have identified approximately 70 common genetic variants across 42 regions ($P<5x10^{-8}$) associated with risk of CRC, as larger study populations have been amassed and racial/ethnic representation has increased [3-11]. Expanded consortium efforts facilitating the discovery of additional risk loci may capture unexplained familial risk.

Our prior collaborative work identified six novel CRC susceptibility loci based on a discovery sample of 18,299 cases and 19,656 controls of European ancestral heritage [12]. Results from this GWAS contributed to the development of the Illumina Infinium® OncoArray-500K BeadChip (OncoArray; San Diego, CA), a genotyping array designed to interrogate genomic variation associated with predisposition to five of the most common cancers (prostate, breast, colorectal, lung, and ovarian) [13]. Here, we describe results from a new discovery-replication GWAS, including for the first time findings from the OncoArray Project. Then, we present a follow-up evaluation of genome-wide statistically significant ($P<5x10^{-8}$) risk alleles in individuals from diverse ethnic groups (East Asian, Hispanic, and African American) to investigate if the findings generalize to other populations. Our goal was to discover and replicate new CRC susceptibility loci by assembling the largest international study population to date (N=163,315).

Methods

Study Overview

This investigation included genetic data from 53 observational studies and clinical trials (**Supplementary Figure 1**, **Supplementary Table 1**). In the discovery stage, we combined genotype and epidemiologic data from individuals with European ancestry from all of our consortium efforts to date (CORECT, CCFR, and GECCO), including the new OncoArray Project (36,948 cases and 30,864 controls; **Supplementary Table 2, Supplementary Figures 2 and 3**). In the replication stage, we leveraged data from an independent set of European-descent participants (12,952 cases and 48,383 controls; **Supplementary Table 3**). In the follow-up stage to assess generalizability of findings, we examined data from a multiethnic sample set (12,085 cases and 22,083 controls) that included East Asians from the OncoArray Project (**Supplementary Table 4, Supplementary Figure 4**) and prior studies [14, 15], African Americans [15, 16], and Hispanics/Latinos [17]. Details of the study populations, genotyping, quality control (QC), and imputation for each stage of this GWAS are described in the **Supplementary Methods**. Participants provided written informed consent and the Institutional Review Boards at each center approved the study. For more specific information on consent and study approvals at each institution, see the Supplementary Methods.

Statistical Analysis

Detailed descriptions of the statistical analysis for each study stage are described in the **Supplementary Methods**. Briefly, we examined the association between allelic dosage for all autosomal variants with MAF ≥0.01 that passed stringent imputation quality control procedures and CRC status using logistic regression adjusted for appropriate study-specific covariates and principal components that capture global ancestry. Summary statistics from European-descent

samples included in our prior consortium efforts (Discovery Part 1)[18] and the OncoArray Project (Discovery Part 2) were combined in a fixed-effect inverse variance-weighted meta-analysis. Consistency of odds ratios (ORs) across studies were assessed using Cochran's *Q* test of heterogeneity. The most statistically significantly associated variant in each novel genome-wide statistically significant (2-sided $P < 5x10^{-8}$) locus from this discovery analysis was then examined for association with risk of CRC in the independent replication stage of European-ancestry participants (**Supplementary Methods**). Criteria for independent replication included a consistent direction of association and $P<0.05$ based on a meta-analysis of study-specific logistic regression models. Finally, all variants reaching genome-wide statistical significance ($P<5x10^{-8}$) in the discovery stage and $P<0.05$ in the replication stage were assessed for generalizability in the multiethnic follow-up stage of East Asians, African Americans, and Hispanics. All statistical tests were two-sided.

Polygenic Risk Scores and Familial Relative Risk Explained

Polygenic risk scores (PRS) in European-descent replication phase participants were calculated using previously known susceptibility variants and novel independently-replicated variants identified by this effort. PRS were categorized into percentile categories based on a weighted sum of risk allele counts among controls (<1%, 1-10%, 10-25%, 25-75%, 75-90%, 90-99%, >99%, with 25-75% serving as the reference). Weights were applied based on bias-corrected logORs from our European-descent discovery analysis. Logistic regression was used to examine CRC risk across PRS categories (after adjusting for age, sex, PCs, and PC*study) for known and known+novel variants, respectively. We also stratified the PRS at a clinically actionable threshold of OR≥2.0. To consider the applicability of our European-derived PRS to

East Asian populations, we also examined the performance of this score in the East Asian cases and controls genotyped on the OncoArray. Next, the contributions to familial risk of the known+novel and the known only variants were investigated. Sample inclusions and methods for bias correction, PRS, and family relative risk explained analyses are described in more detail in the **Supplementary Methods**.

In Silico Functional Follow-up

We conducted eQTL analysis in colonic mucosa from healthy controls (N=50) and normal mucosa adjacent to colon cancer (N=100) in the Colonomics study[19] as well as transverse colon tissues (N=169) from the Genotype-Tissue Expression (GTEx) project (**Supplementary Methods**) [20]. Briefly, in Colonomics, for each variant, Pearson partial correlation adjusted for tissue type (healthy or adjacent to tumor) was used to explore the association of dosage SNP/indel data with gene expression for genes located within 2MB of the SNP of interest. For GTEx, the laboratory and analytic methods have previously been described in detail [20].

Additionally, candidate functional variants were identified using published methods [21]. Briefly, index variants and SNPs (CEU, 1KGP, June 2014 release) in LD with each risk variant (we report $r^2 \geq 0.6$ except where noted as $r^2 \geq 0.2$) were aligned with chromatin immunoprecipitation and sequencing (ChIP-seq) tracks for histone methylation and acetylation marks associated with enhancers H3K4me1 and H3K27ac. For this study, we referenced Sigmoid Colon H3K27 acetylation from the Roadmap Epigenomics Consortium[22] as well as CRC cell lines SW480 and HCT-116 H3K4 monomethylation generated in our laboratory (G. Casey) and from the ENCODE project, respectively [23, 24]. To further characterize the novel

CRC genetic risk loci, we performed *in silico* bioinformatic functional annotation of each region.

Results *Discovery GWAS (European-descent)*

The discovery GWAS identified 11 common risk variants at 4q22.2, 5q15.33, 5p13.1, 6p21.31, 6p12.1, 10q11.23, 12q24.21, 13q13.2, 16q24.1, 20q11.22, and 20q13.13, all of which were independent of known risk loci (>500kb away or r^2>0.2 with a previously known variant) and reached the accepted genome-wide statistical significance threshold ($P<5x10^{-8}$) (**Table 1**). Association results from the discovery stage also indicated that 62 (92.5%) of the 67 known autosomal risk variants (three out of 70 known risk variants were excluded due to MAF<0.01, low quality imputation, or location on chromosome X) replicated at a nominal level of statistical significance ($P<0.05$; **Supplementary Table 5**). A quantile-quantile plot illustrates appropriate control for population stratification with a $\lambda=1.05$ (sample size adjusted $\lambda_{1000}=1.002$; **Supplementary Fig. 5**). A Manhattan plot illustrates the genomic location of novel loci in relation to previously published risk regions (**Figure 1**). Regional association plots in **Supplementary Figure 6** depict the 11 risk variants in the context of their surrounding linkage disequilibrium (LD) structures and nearby genes. The MAFs of these 11 variants in 1KGP Europeans ranged from 0.097 to 0.495, and the ORs for association ranged from 0.90 to 1.08 (**Table 1**). Effect sizes adjusted for potential bias in estimation due to the winner's curse are summarized in **Supplementary Table 6** and **Supplementary Figure 7**.

Replication (European-descent)

The association between each of the 11 candidate susceptibility variants identified in the

discovery stage and risk of CRC in an independent sample revealed consistent directions of association and consistent effect sizes for all variants (**Table 1**). Also, ORs for association were statistically significant for 9 of 11 variants. The remaining two loci that were identified in the discovery stage (rs10161980 and rs2295444) demonstrated supportive but not statistically significant evidence of replication, and thus require further validation in future studies. Notably, the two variants with statistical evidence of heterogeneity in the discovery stage meta-analysis replicated in this independent sample set (rs58791712 and rs2696839).

Multiethnic Follow-up

Subsequently, we examined the 9 novel, replicated risk variants across three diverse ethnic populations. We examined the association between each variant and risk of CRC in East Asians (N=21,630; **Supplementary Fig. 4**), African Americans (N=6,597), and Hispanics (N=5,941). All 9 variants demonstrated a consistent direction of association in follow-up studies except for rs62404968 and rs10994860 in Hispanics (**Table 2**). Eight out of the 9 variants (all but rs10994860) were associated with the risk of CRC in at least 1 population at a nominal level of statistical significance ($P<0.05$).

Polygenic Risk Score Analysis and Familial Relative Risk Explained

PRS analysis conducted in a subset of European-descent replication phase participants revealed that the estimated odds of developing CRC for individuals with scores in the top 1% as compared the 25-75% reference category was 2.18 (**Supplementary Table 7**). Based on the 76 known and novel variants, 4.3% of the study population could be identified for targeted screening based on a clinically actionable threshold of an OR≥2.0 (**Supplementary Table 7**)

[25, 26]. This is in comparison to 1.4% of the study population that is identifiable based on previously known variants only (data not shown). The known + novel PRS performed similarly in East Asians, and the cutpoint to reach a clinically actionable OR of at least 2.0 in this population was 99.1% (**Supplementary Table 7**).

Overall, 76 variants explained 11.9% (95% CI 9.2 – 15.5%) of the known familial relative risk as compared to 10.3% (95% CI 7.9 – 13.7%) for the previously known variants only. This represents a 14.7% increase in familial relative risk explained. Estimation of the proportion of explained familial risk incorporated uncertainty in risk estimation for each variant and uncertainty in the specification of the familial relative risk.

eQTL Analysis

Analysis of *cis* gene expression data for the 9 novel susceptibility variants revealed several noteworthy eQTLs in Colonomics and GTEx transverse colon samples (**Supplementary Table 8**). For example, rs10994860 is a statistically significant eQTL for *ASAH2* (effect size=-0.61; P=5.7E x 10^{-5}). Further, in the Colonomics dataset, rs6906359 is a statistically significant eQTL for several genes including *BRPF3*, showing over-expression for C/C as compared to T/T genotypes (partial r^2=0.09, P=2.6 x 10^{-4}). The most statistically significant eQTLs in each region with at least one variant associated at the P<0.05 level in the Colonomics dataset are summarized in **Supplementary Figure 8**.

Discussion

This collaborative study included over 163,000 individuals for the identification and

further evaluation of 9 replicable novel CRC genetic susceptibility loci. Nine low-penetrance risk loci represent approximately a 21% increase from those previously discovered to date (N=42). Nine risk variants replicated in an independent sample of European-ancestry participants and 8 of those generalized to at least one of three other racial/ethnic populations. Our findings contribute substantially to the known familial relative risk explained by low penetrance susceptibility alleles, with a 14.7% increase from 10.3% (previously known only) to 11.9% (known + novel reported here) explained. Further, PRS analysis underscores the impact of common CRC risk alleles, particularly among individuals with the highest counts of risk variants. Our findings suggest that 4.3% of the population could be targeted for earlier and more frequent screening based on germline genetic profiling of all known common CRC susceptibility variants. This supports our previous findings that GWAS have the potential to inform appropriate tailoring of screening guidelines to population subgroups [27].

The consistent direction of association for all 9 novel risk variants in East Asians and African Americans (all but 2 in Hispanics) underscores the generalizability of our findings from European-ancestry individuals. However, the statistically significant association of some but not all variants with CRC risk across the additional ethnic subgroups supports the importance of expanded sample sizes in certain populations as well as ongoing multiethnic fine-mapping studies to identify the strongest signals and most likely putative functional variant(s) at particular loci in other ancestral populations.

Two of the 9 risk alleles map to intragenic or coding regions. First, rs62404968 maps to 6p12.1 and lies within an intron of *BMP5*. *BMP5* encodes bone morphogenetic protein 5 that is part of the transforming growth factor-beta (TGF-β) superfamily. Members of the BMP and TGF-β family have been implicated as risk genes for CRC in previous GWAS, including *BMP2*

and *BMP4* on chromosomes 20 and 14, respectively [28]. The associated SNP, rs62404968 or any of the 20 SNPs in LD, do not map to any predicted regulatory/enhancer regions based on histone marks suggesting that further functional follow up is needed to understand the functional mechanism likely acting on the strong candidate gene *BMP5*. Second, rs10994860 maps to 10q11.23 and lies within exon 1 of *A1CF*, representing a putative candidate functional SNP. *A1CF* (APOBEC1 Complementation Factor) is a critical component of the apolipoprotein B mRNA editing enzyme complex. There are two SNPs (rs71457593 and rs10994720) in LD with rs10994860 that both map to histone peaks also suggesting potential functionality.

The remaining seven risk alleles map to intergenic regions of the genome. SNP rs1370821 maps to 4q22.2, with the two nearest genes being *ATOH1* and *SMARCAD1* (approximately 85kb away). *ATOH1* encodes atonal homolog BHLH transcription factor 1 that belongs to the basic helix-loop-helix family of transcription factors. *SMARCAD1* encodes Matrix-Associated Actin-Dependent Regulator Of Chromatin, a member of the SNF subfamily of helicase proteins that play an important role in heterochromatin reorganization following DNA replication. While the associated SNP, rs1370821, does not map to any candidate regulatory regions, two SNPs (rs2510787; rs2433324) in LD with rs1370821 lie within an intron of *PDLIM5* (encoding PDZ and LIM domain protein 5), and both map to histone marks. Also, rs1370821 warrants further functional characterization because of its proximity to *BMPR1B*, a gene where there is statistical evidence of an eQTL relationship by genotype in the Colonomics dataset and where the gene family is related to polyposis and CRC susceptibility [17].

The indel rs58791712 (G/GT) maps to 5p13.1. The nearest genes, *PTGER4* and *LINC00603*, lie approximately 400kb from the index variant. *PTGER4* encodes PGE2 Receptor EP4 Subtype and is one of four receptors identified for prostaglandin E2. This indel does not

map to any histone marks making it unlikely to be a functional variant. However, there are three SNPs (rs72748452, rs755989 and rs4957261) in LD with rs58791712 that overlap histone peaks.

The SNP rs2735940 maps to 5p15.33 and lies adjacent to the *TERT* gene. *TERT* encodes the Telomerase Catalytic Subunit protein that helps to maintain telomere ends by addition of the telomere repeat TTAGGG. *TERT* has been identified previously as a candidate risk gene in several cancers including CRC [29-34]. SNP rs2735940 does not map to any histone marks. However, this SNP is in LD with three SNPs (rs380145, rs246995 and rs246994) that map to histone marks and lie within an intron of *CLPTM1L* (rs380145) or the predicted gene *BC034612* (rs246995 and rs246994).

The SNP rs6906359 maps to 6p21.31, and the closest gene is *FKBP5* approximately 12kb away. *FKBP5* encodes FK506 Binding Protein 5, a member of the immunophilin protein family that plays a role in immunoregulation, protein folding, and trafficking. However, rs6906359 does not overlap any histone marks. Of the SNPs in LD with rs6906359 that overlap histone peaks, two SNPs (rs72894781 and rs72894784) map within an intron of *TEAD3*, one SNP (rs16878812) maps within an intron of *FKBP5*, and one SNP is intergenic (rs45493300).

The indel rs72013726 (CACAA/C) maps to 12q24.21. The nearest gene, *MED13L*, lies approximately 500kb from rs72013726. *MED13L* encodes Thyroid Hormone Receptor-Associated Protein 2 and is one of many proteins that function as a transcriptional coactivator for RNA polymerase II-transcribed genes. SNP rs72013726 maps to a histone peak, making it a potential functional SNP.

SNP rs2696839 maps to 16q24.1 and lies 15kb from the predicted gene *LOC146513.* While this SNP does not map to any histone marks, all four SNPs (rs12932862, rs12149163, rs12149501, and rs2665316) in LD with rs2696839 do. Of note, there are several lncRNAs in

this region.

SNP rs1810502 maps to 20q13.13 near the gene *PTPN1*, approximately 70kb away. *PTPN1* encodes Protein-Tyrosine Phosphatase 1B a member of the protein tyrosine phosphatase family. This SNP and 14 other SNPs in LD with rs1810502 map to histone marks, implying the possibility that any one of these 15 SNPs could be functionally relevant to CRC etiology.

Our study design has strengths and limitations. We conducted a rigorous two-stage study with discovery and independent replication in European-descent participants. Further, a major strength is that we utilized data from the independent replication phase to conduct PRS and familial relative risk explained analyses. Of note, despite a 14.7% increase beyond prior knowledge, still <12% of familial relative risk is explained by GWAS-identified alleles including our new 9 loci. Thus, additional efforts are needed to fully explain the genetic architecture of this complex disease, potentially with gene-environment interactions. Space limitations preclude detailed descriptions of eQTL analyses for each SNP. However, we found little or no evidence of the 9 novel index SNPs in relation to gene expression for our speculatively implicated genes. Additional eQTL analyses in expanded normal colon tissue sample sets that examine the full landscape of SNPs in LD with the index SNP may help to elucidate the impact of germline susceptibility loci on gene expression. Future studies will be advantageous to identify rare and intermediate frequency susceptibility alleles through expanded sample size as well as increased racial/ethnic minority inclusion. Multiethnic samples will be useful for fine-mapping known and novel risk regions as well as for identifying population-specific variation. In summary, this GWAS provides insight into the etiologies of CRC and provides a basis for future fine-mapping, functional characterization, and risk modeling research.

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Table 1. Eleven novel low-penetrance risk variants identified from the discovery GWAS (European-descent) with $P<5x10^{-8}$ and their results in an independent replication set.

Locus	EFF/REF allele	rsID:CHR:BP	FRQ_EFF (1KGP EUR)	Discovery (N_{case} = 36,948; $N_{control}$ = 30,864)				Replication (N_{case}=12,952; $N_{control}$=48,383)			
				OR (95%CI)	P*	I^2, %	$P_{heterogeneity}$†	OR (95%CI)	P*	I^2, %	$P_{heterogeneity}$†
4q22.2	T/C	rs1370821:4:94943383	0.401	1.07 (1.04 - 1.09)	4.0×10^{-8}	0	0.58	1.05 (1.02 – 1.08)	0.003	42.1	0.14
5p15.33	A/G	rs2735940:5:1296486	0.511	0.92 (0.89 - 0.94)	3.1×10^{-13}	0	0.59	0.93 (0.90 – 0.96)	3.0×10^{-6}	0	0.75
5p13.1	G/GT	rs58791712:5:40281797‡	0.745	0.91 (0.89 - 0.93)	7.3×10^{-14}	56.7	0.13	0.90 (0.87 – 0.93)	1.1×10^{-9}	28.4	0.24
6p21.31	T/C	rs6906359:6:35528378‡	0.097	0.90 (0.86 - 0.93)	3.4×10^{-8}	0	0.65	0.93 (0.89 – 0.98)	0.005	0	0.55
6p12.1	T/C	rs62404968:6:55714314	0.248	0.92 (0.89 - 0.94)	8.6×10^{-10}	0	0.32	0.94 (0.90 – 0.97)	3.8×10^{-4}	0	0.96
10q11.23	T/C	rs10994860:10:52645424	0.202	0.92 (0.89 - 0.95)	3.5×10^{-8}	0	0.35	0.96 (0.92 – 1.00)	0.04	0	0.43
12q24.21	CACAA/C	rs72013726:12:115890835‡	0.505	0.93 (0.90 - 0.95)	5.0×10^{-11}	0	0.84	0.95 (0.92 – 0.98)	9.1×10^{-4}	0	0.83
13q13.2	C/G	rs10161980:13:34093518	0.620	1.08 (1.05 - 1.10)	4.7×10^{-9}	0	0.81	1.03 (0.99 – 1.06)	0.13	21.6	0.28
16q24.1	C/G	rs2696839:16:86340448	0.495	0.94 (0.92 - 0.96)	2.0×10^{-8}	75.6	0.04	0.96 (0.93 – 0.99)	0.009	25.5	0.25
20q11.22	T/C	rs2295444:20:33173883	0.495	0.93 (0.91 - 0.95)	3.3×10^{-9}	0	0.97	0.97 (0.94 – 1.00)	0.08	0	0.59
20q13.13	T/C	rs1810502:20:49057488	0.449	0.93 (0.91 - 0.96)	1.02×10^{-8}	0	0.98	0.94 (0.91 – 0.97)	5.9×10^{-5}	11.8	0.34

*P values were derived from a fixed-effects inverse variance weighted meta-analysis. All tests were two-sided. Abbreviations: EFF = effect allele; REF = reference allele (reference category for the odds ratios); CHR = chromosome; BP = position; FRQ = frequency; 1KGP EUR = 1000 Genomes Europeans; OR = odds ratio; CI= confidence interval.† P values were derived from Cochran's *Q* test of heterogeneity. All tests were two-sided.
‡ Proxies were used in the independent replication stage (r^2 values from 1KGP Phase 3 Release 5): rs12520534 (chr5:40281761), r^2=1.0; rs144037597 (chr6: 35528204), r^2=1.0; rs12822984 (chr12:115888504), r^2=0.81.

Table 2. Multiethnic follow-up of 9 novel, independently-replicated low-penetrance risk variants

Locus	EFF/REF allele	rsID:CHR:BP	FRQ_EFF (1KGP EAS)	FRQ_EFF (1KGP AMR)	FRQ_EFF (1KGP AFR)	East Asians (OncoArray, ACCC, US-Japan GWAS)				Hispanic/Latinos (HCCS, MEC, SIGMA)		African Americans (AA CRC GWAS)	
						OR (95%CI)	P*	I^2, %	$P_{heterogeneity}$ †	OR (95%CI)	P*	OR (95%CI)	P*
4q22.2	T/C	rs1370821:4:94943383	0.331	0.274	0.065	1.03 (0.99 - 1.08)	0.13	49.6	0.14	1.17 (1.06 - 1.29)	0.001	1.04 (0.92 - 1.17)	0.54
5p15.33	A/G	rs2735940:5:12964486	0.478	0.432	0.521	0.93 (0.87 - 1.00)	0.03	61.2	0.11	0.99 (0.91 - 1.08)	0.84	0.90 (0.83 - 0.98)	0.01
5p13.1	G/GT	rs58791712:5:40281797	0.956	0.765	0.924	0.87 (0.75 - 1.02)	0.09	0	0.57	0.85 (0.77 - 0.94)	0.001	NA	NA
6p21.31	T/C	rs6906359:6:35528378	0.069	0.138	0.141	0.99 (0.91 - 1.07)	0.73	0	0.45	0.82 (0.73 - 0.93)	0.001	0.96 (0.84 - 1.08)	0.47
6p12.1	T/C	rs62404968:6:55714314	0.061	0.133	0.072	0.97 (0.88 - 1.05)	0.44	60	0.08	1.03 (0.90 - 1.17)	0.69	0.85 (0.74 - 0.97)	0.02
10q11.23	T/C	rs10994860:10:52645424	0.047	0.110	0.222	0.97 (0.89 - 1.06)	0.47	51.2	0.13	1.00 (0.87 - 1.16)	0.97	0.99 (0.90 - 1.09)	0.87
12q24.21	CACAA/C	rs72013726:12:115890835	0.643	0.633	0.360	0.92 (0.87 - 0.98)	0.007	53.9	0.14	0.97 (0.89 - 1.06)	0.53	NA	NA
16q24.1	C/G	rs2696839:16:86340448	0.253	0.334	0.293	0.93 (0.89 - 0.98)	0.004	45	0.18	0.90 (0.82 - 0.98)	0.02	0.92 (0.84 - 1.00)	0.06
20q13.13	T/C	rs1810502: 20: 49057488	0.612	0.507	0.545	0.94 (0.90 - 0.98)	0.007	49.2	0.16	0.92 (0.84 - 1.00)	0.05	0.95 (0.88 - 1.03)	0.24

*P values were derived from a fixed-effects inverse variance weighted meta-analysis. All tests were two-sided. Abbreviations: EFF = effect allele; REF = reference allele (reference category for the odds ratios); CHR = chromosome; BP = position; FRQ = frequency; 1KGP = 1000 Genomes; EAS = East Asian; AMR = Ad Mixed American; AFR = African; ACCC = Asia Colorectal Cancer Consortium; GWAS = genome-wide association study; OR = odds ratio; CI= confidence interval; HCCS = Hispanic Colorectal Cancer Study; MEC = Multiethnic Cohort; SIGMA = Slim Initiative in Genomic Medicine for the Americas; AA = African American; CRC = colorectal cancer.

† P values were derived from Cochran's *Q* test of heterogeneity. All tests were two-sided.

Figure Legends

Figure 1. Manhattan plot summarizing the discovery GWAS association results. (N_{case}=36,948; $N_{control}$=30,864). Green = known risk loci (within 500 kilobases (kb) or r^2>0.2 with an index variant); red = novel risk loci (outside 500kb or r^2>0.2 with an index variant).